

Amendments to Specification

Paragraph at page 1, lines 4-7:

This application is a continuation of U.S. Application No. 09/789,054, filed February 20, 2001, pending, which is a continuation-in-part of U.S. Application No. 09/485,558 filed February 11, 2000, pending, which was the national filing of International Application No. PCT/US98/16688 filed August 12, 1998, pending, which claims the benefit of U.S. Provisional Application No. 60/055,865, filed August 15, 1997, now abandoned.

Paragraph at page 6, lines 11-20:

Figures 1A, 1B and 1C depict ~~Figure 1 depicts~~ the amino acid sequence alignment between the Dr1 proteins encoded by the nucleotide sequences derived from corn clone p0117.chclp58r (SEQ ID NO:4), corn clone p0127.cntam51r (SEQ ID NO:6), contig assembled using sequences derived from rice clone rl0n.pk0076.g1 and PCR-generated fragment (SEQ ID NO:10), soybean clone ses2w.pk0043.b3 (SEQ ID NO:14), wheat clone wle1n.pk0106.g11 (SEQ ID NO:20), and wheat clone wre1n.pk0037.b4 (SEQ ID NO:22), and an *Arabidopsis thaliana* Dr1 protein (NCBI GenBank Identifier (GI) No. 1352316; SEQ ID NO:41). Amino acids which are conserved among all and at least two sequences with an amino acid at that position are indicated with an asterisk (*). Dashes are used by the program to maximize alignment of the sequences.

Paragraph at page 6, lines 21-27:

Figures 2A and 2B depict ~~Figure 2 depicts~~ the amino acid sequence alignment between the DRAP1 proteins encoded by the nucleotide sequences derived from corn clone cbn2.pk0039.h8 (SEQ ID NO:28), rice clone rls12.pk0015.e12 (SEQ ID NO:32), soybean clone sdp4c.pk031.p18 (SEQ ID NO:34), and wheat clone wlm1.pk0016.f3 (SEQ ID NO:40), and the *Homo sapiens* DRAP1 protein (NCBI GI No. 7513394; SEQ ID NO:42). Amino acids which are conserved among all and at least two sequences with an amino acid at that position are indicated with an asterisk (*). Dashes are used by the program to maximize alignment of the sequences.

Paragraph at page 14, lines 6-28:

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in

the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410; ~~see also www.ncbi.nlm.nih.gov/BLAST/~~). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Paragraph at page 28, line 32 through page 29, line 10:

cDNA clones encoding proteins involved in regulation of gene expression were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410; ~~see also www.ncbi.nlm.nih.gov/BLAST/~~) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet.* 3:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as

calculated by BLAST are reported herein as “pLog” values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST “hit” represent homologous proteins.

Paragraph at page 32, lines 10-14:

Figures 1A-1C present ~~Figure 1 presents~~ an alignment of the amino acid sequences set forth in SEQ ID NOs:4, 6, 10, 14, 20, and 22, and the *Arabidopsis thaliana* sequence (NCBI GI No. 1352316; SEQ ID NO:41). The data in Table 4 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:4, 6, 10, 14, 20, and 22, and the *Arabidopsis thaliana* sequence (NCBI GI No. 1352316; SEQ ID NO:41).

Paragraph at page 34, lines 8-12:

Figures 2A-2B present ~~Figure 2 presents~~ an alignment of the amino acid sequences set forth in SEQ ID NOs:28, 32, 34, and 40, and the *Homo sapiens* sequence (NCBI GI No. 7513394; SEQ ID NO:42). The data in Table 6 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:28, 32, 34, and 40, and the *Homo sapiens* sequence (NCBI GI No. 7513394; SEQ ID NO:42).